



US-102

SEQUENCE LISTING

<110> Ajinomoto Co. Inc.

<120> Method for Producing L-Amino Acid Using Methylotroph

<130> OP1627/US-102

<140>

<141> 2003-11-

<150> JP 2002-336315

<151> 2002-11-20

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 711

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(711)

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ctt	tta	ctg	tcc	atc	gga	ccg	cag	aat	gta	ctg	gtg	att	aaa	caa	gga	96
Leu	Leu	Leu	Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly	
			20					25					30			
att	aag	cgc	gaa	gga	ctc	att	gcg	ggt	ctt	ctc	gtg	tgt	tta	att	tct	144
Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser	
		35					40					45				
gac	gtc	ttt	ttg	ttc	atc	gcc	ggc	acc	ttg	ggc	gtt	gat	ctt	ttg	tcc	192
Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser	
	50					55					60					
aat	gcc	gcg	ccg	atc	gtg	ctc	gat	att	atg	cgc	tgg	ggt	ggc	atc	gct	240
Asn	Ala	Ala	Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala	
	65				70				75					80		
tac	ctg	tta	tgg	ttt	gcc	gtc	atg	gca	gcg	aaa	gac	gcc	atg	aca	aac	288
Tyr	Leu	Leu	Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn	
				85					90					95		
aag	gtg	gaa	gcg	cca	cag	atc	att	gaa	gaa	aca	gaa	cca	acc	gtg	ccc	336
Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro	
			100					105					110			
gat	gac	acg	cct	ttg	ggc	ggt	tcg	gcg	gtg	gcc	act	gac	acg	cgc	aac	384
Asp	Asp	Thr	Pro	Leu	Gly	Gly	Ser	Ala	Val	Ala	Thr	Asp	Thr	Arg	Asn	
		115					120					125				
cgg	gtg	cgg	gtg	gag	gtg	agc	gtc	gat	aag	cag	cgg	ggt	tgg	gta	aag	432
Arg	Val	Arg	Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys	
	130					135					140					

US-102

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Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
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ttg gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac 528
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
165 170 175
acc gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc 576
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
180 185 190
tgg ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg 624
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
195 200 205
tcc agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg 672
Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
210 215 220
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225 230 235

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<210> 2
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 <212> PRT
 <213> Brevibacterium lactofermentum

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Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
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Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
50 55 60
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
65 70 75 80
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
85 90 95
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
100 105 110
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
115 120 125
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
130 135 140
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
145 150 155 160
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
165 170 175
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
180 185 190
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
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tgtcaaac	gttattcc	taaggggtga	gttggttctta	aggaaagcat	aaaaaaaaa	180										
tgcatacaac	aatcagaacg	gttctgtctg	cttgctttta	atgccatacc	aaacgtacca	240										
ttgagacact	tgtttgcaca	gaggatggcc	c atg ttc acg gga agt	att gtc		292										
			Met Phe Thr Gly Ser	Ile Val												
			1	5												
gcg att gtt act ccg atg gat gaa aaa ggt aat gtc tgt cgg gct agc						340										
Ala Ile Val Thr Pro Met Asp Glu Lys Gly Asn Val Cys Arg Ala Ser																
	10	15	20	25	30											
ttg aaa aaa ctg att gat tat cat gtc gcc agc ggt act tcg gcg atc						388										
Leu Lys Lys Leu Ile Asp Tyr His Val Ala Ser Gly Thr Ser Ala Ile																
	25	30	35	40	45											
gtt tct gtt ggc acc act ggc gag tcc gct acc tta aat cat gac gaa						436										
Val Ser Val Gly Thr Thr Gly Glu Ser Ala Thr Leu Asn His Asp Glu																
	40	45	50	55	60											
cat gct gat gtg gtg atg atg acg ctg gat ctg gct gat ggg cgc att						484										
His Ala Asp Val Val Met Met Thr Leu Asp Leu Ala Asp Gly Arg Ile																
	60	65	70	75	80											
ccg gta att gcc ggg acc ggc gct aac gct act gcg gaa gcc att agc						532										
Pro Val Ile Ala Gly Thr Gly Ala Asn Ala Thr Ala Glu Ala Ile Ser																
	75	80	85	90	95											
ctg acg cag cgc ttc aat gac agt ggt atc gtc ggc tgc ctg acg gta						580										
Leu Thr Gln Arg Phe Asn Asp Ser Gly Ile Val Gly Cys Leu Thr Val																
	90	95	100	105	110											
acc cct tac tac aat cgt ccg tcg caa gaa ggt ttg tat cag cat ttc						628										
Thr Pro Tyr Tyr Asn Arg Pro Ser Gln Glu Gly Leu Tyr Gln His Phe																
	105	110	115	120	125											
aaa gcc atc gct gag cat act gac ctg ccg caa att ctg tat aat gtg						676										
Lys Ala Ile Ala Glu His Thr Asp Leu Pro Gln Ile Leu Tyr Asn Val																
	120	125	130	135	140											
ccg tcc cgt act ggc tgc gat ctg ctc ccg gaa acg gtg ggc cgt ctg						724										
Pro Ser Arg Thr Gly Cys Asp Leu Leu Pro Glu Thr Val Gly Arg Leu																
	140	145	150	155	160											
gcg aaa gta aaa aat att atc gga atc aaa gag gca aca ggg aac tta						772										
Ala Lys Val Lys Asn Ile Ile Gly Ile Lys Glu Ala Thr Gly Asn Leu																
	155	160	165	170	175											
acg cgt gta aac cag atc aaa gag ctg gtt tca gat gat ttt gtt ctg						820										
Thr Arg Val Asn Gln Ile Lys Glu Leu Val Ser Asp Asp Phe Val Leu																
	170	175	180	185	190											
ctg agc ggc gat gat gcg agc gcg ctg gac ttc atg caa ttg ggc ggt						868										
Leu Ser Gly Asp Asp Ala Ser Ala Leu Asp Phe Met Gln Leu Gly Gly																
	185	190	195	200	205											
cat ggg gtt att tcc gtt acg act aac gtc gca gcg cgt gat atg gcc						916										

US-102

His	Gly	Val	Ile	Ser	Val	Thr	Thr	Asn	Val	Ala	Ala	Arg	Asp	Met	Ala		
200					205					210					215		
cag	atg	tgc	aaa	ctg	gca	gca	gaa	gaa	cat	ttt	gcc	gag	gca	cgc	gtt	964	
Gln	Met	Cys	Lys	Leu	Ala	Ala	Glu	Glu	His	Phe	Ala	Glu	Ala	Arg	Val		
				220					225					230			
att	aat	cag	cgt	ctg	atg	cca	tta	cac	aac	aaa	cta	ttt	gtc	gaa	ccc	1012	
Ile	Asn	Gln	Arg	Leu	Met	Pro	Leu	His	Asn	Lys	Leu	Phe	Val	Glu	Pro		
			235					240					245				
aat	cca	atc	ccg	gtg	aaa	tgg	gca	tgt	aag	gaa	ctg	ggt	ctt	gtg	gcg	1060	
Asn	Pro	Ile	Pro	Val	Lys	Trp	Ala	Cys	Lys	Glu	Leu	Gly	Leu	Val	Ala		
		250					255					260					
acc	gat	acg	ctg	cgc	ctg	cca	atg	aca	cca	atc	acc	gac	agt	ggt	cgt	1108	
Thr	Asp	Thr	Leu	Arg	Leu	Pro	Met	Thr	Pro	Ile	Thr	Asp	Ser	Gly	Arg		
	265				270						275						
gag	acg	gtc	aga	gcg	gcg	ctt	aag	cat	gcc	ggt	ttg	ctg	taa			1150	
Glu	Thr	Val	Arg	Ala	Ala	Leu	Lys	His	Ala	Gly	Leu	Leu					
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<210> 4

<211> 292

<212> PRT

<213> Escherichia coli

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			20					25					30				
Ala	Ser	Gly	Thr	Ser	Ala	Ile	Val	Ser	Val	Gly	Thr	Thr	Gly	Glu	Ser		
		35				40					45						
Ala	Thr	Leu	Asn	His	Asp	Glu	His	Ala	Asp	Val	Val	Met	Met	Thr	Leu		
	50				55					60							
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	65				70				75					80			
Ala	Thr	Ala	Glu	Ala	Ile	Ser	Leu	Thr	Gln	Arg	Phe	Asn	Asp	Ser	Gly		
			85					90					95				
Ile	Val	Gly	Cys	Leu	Thr	Val	Thr	Pro	Tyr	Tyr	Asn	Arg	Pro	Ser	Gln		
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Glu	Gly	Leu	Tyr	Gln	His	Phe	Lys	Ala	Ile	Ala	Glu	His	Thr	Asp	Leu		
	115					120					125						
Pro	Gln	Ile	Leu	Tyr	Asn	Val	Pro	Ser	Arg	Thr	Gly	Cys	Asp	Leu	Leu		
	130				135						140						
Pro	Glu	Thr	Val	Gly	Arg	Leu	Ala	Lys	Val	Lys	Asn	Ile	Ile	Gly	Ile		
	145				150				155					160			
Lys	Glu	Ala	Thr	Gly	Asn	Leu	Thr	Arg	Val	Asn	Gln	Ile	Lys	Glu	Leu		
			165					170					175				
Val	Ser	Asp	Asp	Phe	Val	Leu	Leu	Ser	Gly	Asp	Asp	Ala	Ser	Ala	Leu		
		180						185				190					
Asp	Phe	Met	Gln	Leu	Gly	Gly	His	Gly	Val	Ile	Ser	Val	Thr	Thr	Asn		
	195						200					205					
Val	Ala	Ala	Arg	Asp	Met	Ala	Gln	Met	Cys	Lys	Leu	Ala	Ala	Glu	Glu		
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His	Phe	Ala	Glu	Ala	Arg	Val	Ile	Asn	Gln	Arg	Leu	Met	Pro	Leu	His		
225					230				235						240		

US-102

Asn	Lys	Leu	Phe	Val	Glu	Pro	Asn	Pro	Ile	Pro	Val	Lys	Trp	Ala	Cys
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Lys	Glu	Leu	Gly	Leu	Val	Ala	Thr	Asp	Thr	Leu	Arg	Leu	Pro	Met	Thr
			260					265					270		
Pro	Ile	Thr	Asp	Ser	Gly	Arg	Glu	Thr	Val	Arg	Ala	Ala	Leu	Lys	His
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US-102

<212> DNA
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US-102

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<223> Description of Artificial Sequence: primer

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